AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

- 1. **(Original)** A process for producing an antibody composition using a cell, which comprises using a cell into which a double-stranded RNA comprising an RNA selected from the following (a) or (b) and its complementary RNA is introduced:
- (a) an RNA comprising the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30;
- (b) an RNA consisting of a nucleotide sequence in which one or several nucleotide(s) is/are deleted, substituted, inserted and/or added in the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30 and having activity of suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain.
- 2. **(Original)** The process according to claim 1, wherein the enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in the complex type N-glycoside-linked sugar chain is α 1,6-fucosyltransferase.

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- 3. (Original) The process according to claim 2, wherein the α1,6-fucosyltransferase is a protein encoded by a DNA selected from the group consisting of the following (a) to (h):
- (a) a DNA comprising the nucleotide sequence represented by SEQ ID NO:1;
- (b) a DNA comprising the nucleotide sequence represented by SEQ ID NO:2;
- (c) a DNA comprising the nucleotide sequence represented by SEQ ID NO:3;
- (d) a DNA comprising the nucleotide sequence represented by SEQ ID NO:4;
- (e) a DNA which hybridizes with a DNA consisting of the nucleotide sequence represented by SEQ ID NO:1 under stringent conditions and encodes a protein having α1,6-fucosyltransferase activity;
- (f) a DNA which hybridizes with a DNA consisting of the nucleotide sequence represented by SEQ ID NO:2 under stringent conditions and encodes a protein having α 1,6-fucosyltransferase activity;
- (g) a DNA which hybridizes with a DNA consisting of the nucleotide sequence represented by SEQ ID NO:3 under stringent conditions and encodes a protein having α1,6-fucosyltransferase activity;
- (h) a DNA which hybridizes with a DNA consisting of the nucleotide sequence represented by SEQ ID NO:4 under stringent conditions and encodes a protein having α 1,6-fucosyltransferase activity.

- 4. (Original) The process according to claim 2, wherein the α1,6-fucosyltransferase is a protein selected from the group consisting of the following
 (a) to (I):
- (a) a protein comprising the amino acid sequence represented by SEQ ID NO:5;
- (b) a protein comprising the amino acid sequence represented by SEQ ID NO:6;
- (c) a protein comprising the amino acid sequence represented by SEQ ID NO:7;
- (d) a protein comprising the amino acid sequence represented by SEQ ID NO:8;
- (e) a protein consisting of an amino acid sequence in which one or more amino acid(s) is/are deleted, substituted, inserted and/or added in the amino acid sequence represented by SEQ ID NO:5 and having α1,6-fucosyltransferase activity;
- (f) a protein consisting of an amino acid sequence in which one or more amino acid(s) is/are deleted, substituted, inserted and/or added in the amino acid sequence represented by SEQ ID NO:6 and having α 1,6-fucosyltransferase activity;
- (g) a protein consisting of an amino acid sequence in which one or more amino acid(s) is/are deleted, substituted, inserted and/or added in the amino acid sequence represented by SEQ ID NO:7 and having α 1,6-fucosyltransferase activity;
- (h) a protein consisting of an amino acid sequence in which one or more amino acid(s) is/are deleted, substituted, inserted and/or added in the amino acid sequence represented by SEQ ID NO:8 and having α 1,6-fucosyltransferase activity;
- (i) a protein consisting of an amino acid sequence which has 80% or more homology to the amino acid sequence represented by SEQ ID NO:5 and having α 1,6-fucosyltransferase activity;

- (j) a protein consisting of an amino acid sequence which has 80% or more homology to the amino acid sequence represented by SEQ ID NO:6 and having α 1,6-fucosyltransferase activity;
- (k) a protein consisting of an amino acid sequence which has 80% or more homology to the amino acid sequence represented by SEQ ID NO:7 and having α 1,6-fucosyltransferase activity;
- (I) a protein consisting of an amino acid sequence which has 80% or more homology to the amino acid sequence represented by SEQ ID NO:8 and having α 1,6-fucosyltransferase activity.
- 5. (Currently Amended) The process according to any one of claims 1-to 4, wherein the cell into which the RNA having activity of suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain is introduced is a cell which is resistant to a lectin which recognizes a sugar chain structure in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in an N-glycoside-linked sugar chain.
- 6. **(Original)** The process according to claim 5, wherein the cell is resistant to at least one lectin selected from the group consisting of the following (a) to (d):
- (a) a *Lens culinaris* lectin;

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(g)

(h)

(i)

(b) a Pisum sativum lectin; (c) a Vicia faba lectin; (d) an Aleuria aurantia lectin. 7. (Currently Amended) The process according to any one of claims 1-to 6, wherein the cell is selected from the group consisting of a yeast cell, an animal cell, an insect cell and a plant cell. 8 (Currently Amended) The process according to any one of claims 1-to 7, wherein the cell is a cell selected from the group consisting of the following (a) to (i): (a) a CHO cell derived from Chinese hamster ovary tissue; (b) a rat myeloma cell line YB2/3HL.P2.G11.16Ag.20 cell; (c) a mouse myeloma cell line NS0 cell; (d) a mouse myeloma cell line SP2/0-Ag14 cell; (e) a BHK cell derived from Syrian hamster kidney tissue; (f) an antibody-producing hybridoma cell;

a human leukemia cell line Namalwa cell;

an embryonic stem cell;

a fertilized egg cell.

- 9. (Currently Amended) The process according to any one of claims 1-to 8, wherein the cell is a transformant into which a gene encoding an antibody molecule is introduced.
- 10. **(Original)** The process according to claim 9, wherein the antibody molecule is selected from the group consisting of the following (a) to (d):
- (a) a human antibody;
- (b) a humanized antibody;
- (c) an antibody fragment comprising the Fc region of (a) or (b);
- (d) a fusion protein comprising the Fc region of (a) or (b).
- 11. (Currently Amended) The process according to claim 9-or 10, wherein the antibody molecule belongs to an IgG class.
- 12. (Currently Amended) The process according to any one of claims 1-to 11, wherein the antibody composition is an antibody composition having higher antibody-dependent cell-mediated cytotoxic activity than an antibody composition produced by a parent cell into which a double-stranded RNA comprising an RNA selected from the following (a) or (b) and its complementary RNA is not introduced:
- (a) an RNA comprising the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30;

- (b) an RNA consisting of a nucleotide sequence in which one or several nucleotide(s) is/are deleted, substituted, inserted and/or added in the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30 and having activity of suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain.
- 13. **(Original)** The process according to claim 12, wherein the antibody composition having higher antibody-dependent cell-mediated cytotoxic activity is an antibody composition which comprises antibody molecules having complex type N-glycoside-linked sugar chains in the Fc region, and in which a ratio of sugar chains in which fucose is not bound to N-acetylglucosamine in the reducing end in the sugar chains among the complex type N-glycoside-linked sugar chains is higher than that of an antibody composition produced by the parent cell.
- 14. (**Original**) The process according to claim 13, wherein the complex type N-glycoside-linked sugar chains are sugar chains in which 1-position of fucose is not bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in the sugar chains.
- 15. (Currently Amended) The process according to any one of claims 12 to 14, wherein the antibody composition having higher antibody-dependent cell-mediated

cytotoxic activity is an antibody composition which comprises antibody molecules having complex type N-glycoside-linked sugar chains in the Fc region, and in which the ratio of sugar chains in which fucose is not bound to N-acetylglucosamine in the reducing end in the sugar chains among the complex type N-glycoside-linked sugar chains is 20% or more.

- 16. (Currently Amended) The process according to any one of claims 12-to 15, wherein the antibody composition having higher antibody-dependent cell-mediated cytotoxic activity is an antibody composition which comprises antibody molecules having complex type N-glycoside-linked sugar chains in the Fc region, and in which the complex type N-glycoside-linked sugar chains are sugar chains in which fucose is not bound to N-acetylglucosamine in the reducing end.
- 17. (Currently Amended) A cell into which an RNA capable of suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain is introduced, and which is used in the process according to any one of claims 1-to 16.
- 18. **(Original)** The cell according to claim 17, wherein the enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position

of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain is α 1,6-fucosyltransferase.

- 19. (Original) A cell in which an RNA selected from RNAs of the group consisting of the nucleotide sequences represented by any one of SEQ ID NOs:9 to 30 is introduced or expressed.
- 20. **(Original)** A double-stranded RNA consisting of an RNA selected from the following (a) or (b) and its complementary RNA:
- (a) an RNA comprising the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30;
- (b) an RNA consisting of a nucleotide sequence in which one or several nucleotide(s) is/are deleted, substituted, inserted and/or added in the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30 and having activity of suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain.
- 21. (Original) A DNA corresponding to the RNA described in claim 20 and a complementary DNA to the DNA.

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- 22. (Original) A recombinant DNA which is obtainable by introducing a DNA corresponding to the RNA described in claim 20 and a complementary DNA to the DNA into a vector.
- 23. **(Currently Amended)** The recombinant DNA according to claim 22, which expresses the double-stranded RNA-according to claim 20 consisting of an RNA selected from the following (a) or (b) and its complementary RNA:
- (a) an RNA comprising the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30;
- (b) an RNA consisting of a nucleotide sequence in which one or several nucleotide(s) is/are deleted, substituted, inserted and/or added in the nucleotide sequence represented by any one of SEQ ID NOs:9 to 30 and having activity of suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α-bond in a complex type N-glycoside-linked sugar chain.
- 24. (Currently Amended) A transformant which is obtainable by introducing the recombinant DNA according to claim 22 or 23 into a cell.
- 25. (**Original**) A method for constructing a cell which is resistant to a lectin which recognizes a sugar chain structure in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type

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N-glycoside-linked sugar chain, which comprises introducing or expressing the doublestranded RNA described in claim 20 in a cell.

- 26. (**Original**) The method according to claim 25, wherein the cell which is resistant to a lectin which recognizes a sugar chain structure in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain is resistant to at least one lectin selected from the group consisting of the following (a) to (d):
- (a) a *Lens culinaris* lectin;
- (b) a *Pisum sativum* lectin;
- (c) a Vicia faba lectin;
- (d) an Aleuria aurantia lectin.
- 27. (Original) A method for suppressing the function of an enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to 6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain, which comprises using an RNA selected from RNAs of the group consisting of the nucleotide sequences of any one of SEQ ID NOs:9 to 30.
- 28. **(Original)** The method according to claim 27, wherein the enzyme relating to the modification of a sugar chain in which 1-position of fucose is bound to

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6-position of N-acetylglucosamine in the reducing end through α -bond in a complex type N-glycoside-linked sugar chain is α 1,6-fucosyltransferase.